

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Chicheportiche, Yves
Browning, Jeffrey L.
- (ii) TITLE OF INVENTION: A TUMOR NECROSIS FACTOR RELATED LIGAND
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BIOGEN, INC.
 - (B) STREET: 14 CAMBRIDGE CENTER
 - (C) CITY: CAMBRIDGE
 - (D) STATE: MA
 - (E) COUNTRY: US
 - (F) ZIP: 02142
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: not yet assigned
 - (B) FILING DATE: 07-May-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: FLYNN, KERRY A.
 - (B) REGISTRATION NUMBER: 33,693
 - (C) REFERENCE/DOCKET NUMBER: A003 PCT CIP
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 679-3583
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: TNF family related protein
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

G GTG CTG AGC CTG GGC CTG GCG CTG GCC TGC CTT GGC CTC CTG CTG
46
Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu
1 5 10 15

GTC GTG GTC AGC CTG GGG AGC TGG GCA ACG CTG TCT GCC CAG GAG CCT
94
Val Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro
20 25 30

TCT CAG GAG GAG CTG ACA GCA GAG GAC CGC CGG GAG CCC CCT GAA CTG
142
Ser Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu
35 40 45

AAT CCC CAG ACA GAG GAA AGC CAG GAT GTG GTA CCT TTC TTG GAA CAA
190
Asn Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln
50 55 60

CTA GTC CGG CCT CGA AGA AGT GCT CCT AAA GGC CGG AAG GCG CGG CCT
238
Leu Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro
65 70 75

CGC CGA GCT ATT GCA GCC CAT TAT GAG GTT CAT CCT CGG CCA GGA CAG
286
Arg Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln
80 85 90 95

GAT GGA GCA CAA GCA GGT GTG GAT GGG ACA GTG AGT GGC TGG GAA GAG
334
Asp Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu
100 105 110

ACC AAA ATC AAC AGC TCC AGC CCT CTG CGC TAC GAC CGC CAG ATT GGG
382
Thr Lys Ile Asn Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly
115 120 125

GAA TTT ACA GTC ATC AGG GCT GGG CTC TAC TAC CTG TAC TGT CAG GTG
430
Glu Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val
130 135 140

CAC TTT GAT GAG GGA AAG GCT GTC TAC CTG AAG CTG GAC TTG CTG GTG
478
His Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val
145 150 155

AAC GGT GTG CTG GCC CTG CGC TGC CTG GAA GAA TTC TCA GCC ACA GCA
526
Asn Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala
160 165 170 175

GCA AGC TCT CCT GGG CCC CAG CTC CGT TTG TGC CAG GTG TCT GGG CTG
574

Ala Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu
 180 185 190
 TTG CCG CTG CGG CCA GGG TCT TCC CTT CGG ATC CGC ACC CTC CCC TGG
 622
 Leu Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp
 195 200 205
 GCT CAT CTT AAG GCT GCC CCC TTC CTA ACC TAC TTT GGA CTC TTT CAA
 670
 Ala His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln
 210 215 220
 GTT CAC TGAGGGGCCT TGCTCTCCCA GATTCTTAA ACTTTCCCTG GCTCCAGGAG
 726
 Val His
 225
 CATCACCAACA CCTCCCTACC CCACCCCCAC TCCTCCACCC CCTCGCTGCT CCTTGGTCCA
 786
 GTCCTGTCTC TCCTCAAAGG CAGCCAGAGC TTGTTCACAT GTTCCATTC CACAGACGTA
 846
 TCCTTGCTCT TCTAACATC CCATCCCACC ACAACTATCC ACCTCACTAG CTCCCAAAGC
 906
 CCCTACTTAT CCCTGACTCC CCCACCCACT CACCCGACCA CGTGTATT GACTTTGTGC
 966
 ACCAGGCACT GAGATGGCT GGACCTGGTG GCAGGAAGCC AGAGAACCTG GGACTAGGCC
 1026
 AGAAGTTCCC AACTGTGAGG GGGAAAGAGCT GGGGACAAGC TCCTCCCTGG ATCCCTGTGG
 1086
 ATTTTAAAAA GATACTATTT TTATTATTAT TGTGACAAAAA TGTTAAATGG ATATTAAAGA
 1146
 GAATAAAATCA TGATTTCTCT TC
 1168

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Val
 1 5 10 15
 Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro Ser
 20 25 30
 Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu Asn

35

40

45

Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln Leu
50 55 60

Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro Arg
65 70 75 80

Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp
85 90 95

Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Thr
100 105 110

Lys Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly Glu
115 120 125

Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His
130 135 140

Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asn
145 150 155 160

Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala
165 170 175

Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu
180 185 190

Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala
195 200 205

His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val
210 215 220

His
225

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: TNF family related protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCA TTG TTA GAC TTT GAA ATT TCC GCC CGC CGG CTC CCC CTC CCC
48
Met Ser Leu Leu Asp Phe Glu Ile Ser Ala Arg Arg Leu Pro Leu Pro
1 5 10 15

CGA TCC CTC GGG TCC CGG GAT GGG GGG GCG GTG AGG CAG GCA CAG CCC
96
Arg Ser Leu Gly Ser Arg Asp Gly Gly Ala Val Arg Gln Ala Gln Pro
20 25 30

CCC GCC CCC ATG GCC GCC CGT CGG AGC CAG AGG CGG AGG GGG CGC CGG
144
Pro Ala Pro Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg
35 40 45

GGG GAG CCG GGC ACC GCC CTG CTG GTC CCG CTC GCG CTG GGC CTG GGC
192
Gly Glu Pro Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly
50 55 60

CTG GCG CTG GCC TGC CTC CGC CTC CTG CTG GCC GTG GTC AGT TTG GGG
240
Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly
65 70 75 80

AGC CGG GCA TCG CTG TCC GCC CAG GAG CCT GCC CAG GAG GAG CTG GTG
288
Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val
85 90 95

GCA GAG GAG GAC CAG GAC CCG TCG GAA CTG AAT CCC CAG ACA GAA GAA
336
Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu
100 105 110

AGC CAG GAT CCT GCG CCT TTC CTG AAC CGA CTA GTT CGG CCT CGC AGA
384
Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg
115 120 125

AGT GCA CCT AAA GGC CGG AAA ACA CGG GCT CGA AGA GCG ATC GCA GCC
432
Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala
130 135 140

CAT TAT GAA GTT CAT CCA CGA CCT GGA CAG GAC GGA GCG CAG GCA GGT
480
His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly
145 150 155 160

GTG GAC GGG ACA GTG AGT GGC TGG GAG GAA GCC AGA ATC AAC AGC TCC
528
Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn Ser Ser
165 170 175

AGC CCT CTG CGC TAC AAC CGC CAG ATC GGG GAG TTT ATA GTC ACC CGG
576
Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg
180 185 190

GCT GGG CTC TAC TAC CTG TAC TGT CAG GTG CAC TTT GAT GAG GGG AAG
 624
 Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys
 195 200 205

 GCT GTC TAC CTG AAG CTG GAC TTG CTG GTG GAT GGT GTG CTG GCC CTG
 672
 Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu
 210 215 220

 CGC TGC CTG GAG GAA TTC TCA GCC ACT GCG GCC AGT TCC CTC GGG CCC
 720
 Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro
 225 230 235 240

 CAG CTC CGC CTC TGC CAG GTG TCT GGG CTG TTG GCC CTG CGG CCA GGG
 768
 Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly
 245 250 255

 TCC TCC CTG CGG ATC CGC ACC CTC CCC TGG GCC CAT CTC AAG GCT GCC
 816
 Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala
 260 265 270

 CCC TTC CTC ACC TAC TTC GGA CTC TTC CAG GTT CAC TGAGGGGCC
 862
 Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His
 275 280

 TGGTCTCCCC ACAGTCGTCC CAGGCTGCCG GCTCCCCTCG ACAGCTCTCT GGGCACCCGG
 922

 TCCCCCTCTGC CCCACCCCTCA GCGGCTCTTT GCTCCAGACCC TGCCCCCTCCC TCTAGAGGCT
 982

 GCCTGGGCCT GTTCACGTGT TTTCCATCCC ACATAAATAC AGTATTCCCA CTCTTATCTT
 1042

 ACAACTCCCC CACCGCCCCAC TCTCCACCTC ACTAGCTCCC CAATCCCTGA CCCTTGAGG
 1102

 CCCCCAGTGA TCTCGACTCC CCCCTGGCCA CAGACCCCCA GGGCATTGTG TTCACTGTAC
 1162

 TCTGTGGGCA AGGATGGGTC CAGAAGACCC CACTTCAGGC ACTAAGAGGG GCTGGACCTG
 1222

 GCGGCAGGAA GCCAAAGAGA CTGGGCCTAG GCCAGGAGTT CCCAAATGTG AGGGGCGAGA
 1282

 AACAAAGACAA GCTCCTCCCT TGAGAATTCC CTGTGGATTT TTAAAACAGA TATTATTTT
 1342

 ATTATTATTG TGACAAAATG TTGATAAATG G
 1373

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Leu Leu Asp Phe Glu Ile Ser Ala Arg Arg Leu Pro Leu Pro
1 5 10 15

Arg Ser Leu Gly Ser Arg Asp Gly Gly Ala Val Arg Gln Ala Gln Pro
20 25 30

Pro Ala Pro Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg
35 40 45

Gly Glu Pro Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly
50 55 60

Leu Ala Leu Ala Cys Leu Gly Leu Leu Ala Val Val Ser Leu Gly
65 70 75 80

Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val
85 90 95

Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu
100 105 110

Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg
115 120 125

Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala
130 135 140

His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly
145 150 155 160

Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn Ser Ser
165 170 175

Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg
180 185 190

Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys
195 200 205

Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu
210 215 220

Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro
225 230 235 240

Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly
245 250 255

Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala
260 265 270

Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His
275 280